

Supplementary Table 1. Detailed correctness analysis for all assemblies of *Staphylococcus aureus*, *Rhodobacter sphaeroides*, and human chr. 14. Column headers are as follows. Genome size: the true genome size for the bacteria, and the ungapped true genome size for human. Assembly size: the total size of all contigs >200bp. Chaff size: the size of all “chaff” contigs as defined in the main text. Contig ES: E-size of contigs as defined in the main text. Contig AES: adjusted E-size after breaking all contigs at every misjoin and every indel >5bp. Contig N50: N50 size of contigs based on known genome size. Contig AN50: Adjusted N50 size after breaking all contigs at every misjoin and every indel >5bp. Scaffold N50: N50 size of scaffolds based on known genome size. Unaligned ref bases: total number of bases from the reference for which no contig matched. Unaligned asm bases: total number of bases in the assembly that failed to align to the reference. Duplicated ref bases: total number of bases that occurred in more copies than exist in the reference. Compressed ref bases: total number of bases that occurred in too few copies in the assembly. Bad trim: total number of bases on the ends of contigs that fail to match the reference. SNPs: single nucleotide polymorphisms, i.e., one-base mismatches compared to the reference. Indels: insertions and deletions with respect to the reference. Misjoins: locations where two adjacent sequences in the assembly should be split apart and placed at distinct locations in order to match the reference. Inversion: a misjoin where a segment needs to be flipped to match the reference. Relocation: a misjoin where a segment needs to be moved elsewhere on the chromosome. Translocation: a misjoin where a segment needs to be moved to another chromosome. Note that human chromosome 14, as a single chromosome, could not yield any translocations. *S. aureus* has 2 small plasmids and one large chromosome. *Rhodobacter* has 2 chromosomes plus 5 plasmids.

Assembly	Genome size	Assembly size	Chaff size	Contig		Contig		Scaffold		Unaligned ref bases	Unaligned asin bases	Duplicated ref bases	Compressed ref bases	Bad Average	Indels	Contigs				Scaffolds															
				ES	AS	MSD	ANSO	MSD	ANSO							MSD	ANSO	Highly	Everson	Relocation	Translocation	Total	Inversion	Indel/Relocation	Translocation										
S. aureus																																			
ATCC	2901081	3847346	125.64%	189957	6.54%	43124	114023	72.82%	29198	24819	83.00%	34376	77917	81.48%	39428	1.36%	170	669882	23.06%	28367	0.98%	53	99.97	258	20	9	5	3	2	-	1	1	0	-	
ALPATHS-LG	2901081	2899869	98.86%	907	0.03%	110936	50078	81.20%	96740	66230	68.46%	1091731	1091731	100.00%	17946	0.52%	189	792	0.03%	36005	1.26%	161	99.99	79	4	12	4	0	4	-	0	0	0	-	
BamBuz	2901081	2833735	97.61%	0	0.00%	60996	19610	28.38%	50192	45701	31.28%	1083792	1083792	100.00%	37383	1.30%	43	171	0.01%	36961	1.27%	9	99.99	28	56	164	13	2	11	-	0	0	0	-	
MSR-CA	2901081	2862000	98.58%	552	0.02%	60448	50381	83.35%	99152	48234	81.54%	2411914	1021905	42.37%	37340	1.29%	27	23895	0.82%	28896	1.00%	27	99.97	191	23	10	12	6	6	-	3	3	0	-	
SGA	2901081	2833736	97.61%	614338	21.16%	4726	4712	99.69%	4005	3995	99.75%	-	-	-	54955	1.89%	136	850	0.03%	37211	1.28%	108	100	32	2	2	4	1	3	-	-	-	-	-	
SOApendov	2901081	2909124	100.21%	10156	0.35%	232352	88802	26.95%	288184	62681	21.75%	331598	284904	85.67%	10839	0.37%	315	41277	1.42%	40437	1.39%	284	99.96	246	25	31	17	1	16	-	8	1	7	-	
Velvet	2901081	2847738	98.08%	12971	0.45%	60234	48511	89.42%	48440	21460	85.61%	762333	126167	16.52%	23068	0.78%	894	7899	0.19%	36772	1.27%	144	99.98	217	6	14	14	5	9	-	17	5	12	-	
S. pharaonides																																			
ATCC	4601060	4669251	107.96%	76138	1.65%	9356	6877	73.51%	5872	4213	71.85%	8859	4599	51.91%	118484	1.01%	6355	462897	10.94%	20134	0.44%	6678	99.97	692	288	34	21	2	14	5	3	0	1	0	
ALPATHS-LG	4601060	4587828	99.84%	548	0.01%	44816	35973	89.59%	42455	34424	81.09%	2192334	2192334	100.00%	21664	0.47%	444	17262	0.38%	13816	0.30%	60	99.98	218	150	37	6	0	3	3	0	0	0	0	-
BamBuz	4601060	4371571	94.97%	0	0.00%	94521	14281	17.22%	93198	12781	13.72%	2438507	2418500	99.18%	224768	4.93%	211	1749	0.05%	10963	0.24%	78	99.99	189	149	363	5	0	3	2	2	0	0	1	1
CABOG	4601060	4238067	92.07%	125	0.00%	24066	21539	89.50%	20211	17968	88.41%	65690	5312	84.20%	244543	7.50%	526	6478	0.14%	23050	0.70%	483	99.96	536	145	24	10	1	2	7	5	4	0	1	-
MSR-CA	4601060	4465002	97.00%	830	0.02%	24214	21579	89.12%	22128	19985	86.25%	2975004	2967689	99.74%	161815	1.52%	1775	47991	1.04%	22341	0.49%	1658	99.97	807	179	32	10	1	5	4	5	2	0	3	0
SGA	4601060	4502862	97.82%	22778	4.90%	4078	4061	99.79%	2861	2854	99.76%	-	-	-	106250	2.11%	871	2740	0.08%	42285	0.92%	856	99.99	338	118	4	4	0	2	2	-	-	-	-	-
SOApendov	4601060	4596074	99.85%	20523	0.45%	157153	18553	11.81%	131681	14340	10.89%	666165	657636	99.62%	40615	0.88%	481	40134	1.07%	23493	0.51%	121	99.97	527	155	406	8	0	4	4	3	0	1	2	0
Velvet	4601060	4503268	97.83%	24985	0.54%	18552	16731	90.08%	15652	14482	92.45%	353027	270086	76.51%	73852	1.60%	316	13176	0.29%	42569	0.92%	193	99.98	413	148	27	8	0	6	2	19	6	6	2	7
S. maritimus																																			
ATCC	88289540	73341066	83.07%	3652835	41.37%	3291	3134	95.23%	2024	1956	96.64%	2129	2039	94.83%	1569432	17.78%	27144	520979	0.59%	460918	0.52%	14752	99.9	60488	9987	678	13	6	7	-	9	9	0	-	
ALPATHS-LG	88289540	84436099	95.63%	2366	0.00%	47031	57749	57.74%	36530	21042	57.61%	8164636	4702139	5.76%	2440622	2.76%	30060	238667	0.27%	2269633	2.57%	18473	99.84	53317	27559	2598	101	44	57	-	45	0	45	-	
BamBuz	88289540	68248005	77.29%	153	0.00%	23291	15461	27.24%	3851	4322	73.87%	242089	164446	69.28%	18139626	20.53%	60387	127459	0.14%	3568313	4.04%	43775	99.86	64869	17141	5411	3366	172	1544	-	143	37	106	-	
CABOG	88289540	8623273	97.67%	24446	0.03%	98793	30689	53.20%	46356	23707	52.29%	392605	25992	6.59%	1487019	1.68%	54956	139908	0.16%	1509716	1.71%	20823	99.85	8126	28420	2883	149	46	103	-	597	389	208	-	
MSR-CA	88289540	83291273	94.34%	289271	3.33%	6762	5927	87.66%	4906	4247	88.61%	893428	89668	10.48%	5307963	6.01%	550163	1499562	1.43%	2218738	2.51%	349266	99.71	142268	21800	2161	1374	811	93	-	1668	210	858	-	
SGA	88289540	82375466	93.30%	9515354	107.82%	3795	3771	98.49%	2710	2671	98.56%	-	-	-	6158062	9.97%	53663	135547	0.14%	1888332	2.14%	32693	99.89	7076	15483	681	150	90	60	-	268	17	251	-	
SOApendov	88289540	9260368	104.89%	3331511	3.77%	33023	38801	50.98%	14724	7442	50.54%	455068	214392	47.11%	1619458	18.03%	527247	996461	6.76%	3319777	3.79%	317934	99.81	88165	23147	2902	1061	520	741	-	389	199	170	-	
Velvet	88289540	74740589	84.65%	5519204	6.25%	3276	3049	93.09%	2294	2139	93.24%	1190421	27052	2.27%	1348795	15.12%	273461	83574	0.04%	568790	0.64%	89590	99.86	79399	17505	4172	268	199	170	-	9156	3824	5332	-	